

A

Sequence alignment of A.th. APP and Z.m. NAP. The alignment shows three conserved regions: A, B, and C. Region A is located at the N-terminus, region B in the middle, and region C at the C-terminus. Conserved amino acids are indicated by dots above the sequence, and gaps are shown as dashes.

	A.th. APP	Z.m. NAP	Region
1	MSA R E K P D E I R K S A E R G H S T G M K A V S E H E E A E A E K A V V A A A P T S V A N G Y D V A V	PT K D E E S K D G K R E M C G N	B
47	S K R K R H N - S S N D I T Y E S N K L I A N G E F R G M I V K E L R E E A I K R G M D A N T S T N K Q D E E S C M D A N N V S I A P V K	N K R K R H S I G D G G E E G N G D I T C T D M V K L E G M S Y R E H O G L A K A R G M A N N E G N G K V H O S H L S I A T A G P V A A V D G	112
113	S S N E I D E E D D N N G F E E E X E E K E V V V	G P L S E A K E N V I K G G D E E E M V E K E E K V V V	C
135			
		138	
		159	

B

M.m. ADPRT	1	A E T S E P I Y R V Q M A K G S I G R A S S C I K S E S P I D C S H I S P I D I V O D S P M E P G K V P H H Y V H E S F W K V G Q S I S H P T	Zn - finger I		
Z.m. ZAP	1	M A A P P P X I A W K A E V A K S G I G R A S S C I K S G R S P I A K D O G R G K M V A O S I O D G F M P M W N H A			56
Z.m. ZAP(race)	1	M A A P P P X I A W K A E V A K S G I G R A S S C I K S G R S P I A K D O G R G K M V A O S I O D G F M P M W N H A R C I F S K K N Q I S V D			67
M.m. ADPRT	68	V E N D G E S E R P W D L D O K V K R T A E G			
Z.m. ZAP	57	- D A V E G I D A L D A R W D D I D O E K F E B N Y V I			
Z.m. ZAP(race)	68	- D A V E G I D A L D A R W D D I D O E K F E B N Y V I - - - G S A S A G T S S T A 98			115
		Zn - finger II			
M.m. ADPRT	135	Q M H E S K I V D P P E X K O L G M I D R W A Y P T T E V V K K R			
Z.m. ZAP	116	S V E T T S A S S E I E S E G B X . E B - - P W Y H A N C E V S P S A T V E K F S G W D T E S D E D K R M L D E V V K K D M G N M			190
		NLS			178
M.m. ADPRT	191	K E A I L K O L P A - - I M N E G K R K G D E V G T D E P K			
Z.m. ZAP	179	N K A S K E K K S E N D I D O S Y K S A M L E S T S E G T D E K			251
		NLS			245
M.m. ADPRT	252	X K A C S H N D E K S A H I F N O C V P S G E S A K W H M V A U S H A P A			
Z.m. ZAP	246	X T H V S A A E K R D M T E A N G S D T S G P E R H A M W R C A D C M I			318
		DNA - binding domain			312
M.m. ADPRT	319	K C M V K M O N S S V - - K E W V T H			
Z.m. ZAP	313	K C M V S A T I E V N K K M D I P H G T K D N D Y L I N K W F K S O V A K K P E T A L			380
		auto -			
		modification domain			
M.m. ADPRT	381	S S P A A D S P P S N M K I L T E E K L S O N K D E A K A V I E K L E G K L T G S A N A S L C I S I K K E V E K M K K M E E V K E			
Z.m. ZAP	371	S S P A A D S P P S N M K I L T E E K L S O N K D E A K A V I E K L E G K L T G S A N A S L C I S I K K E V E K M K K M E E V K E			447
M.m. ADPRT	448	A N D R V V S E D D F D O V S A S T S S O S A H M L S P W A V E V K A E P G E V V A P R G K S A A P S K K S K G C F K E			
Z.m. ZAP	438	L K H P V V M S E D D F D O V S A S T S S O S A H M L S P W A V E V K A E P G E V V A P R G K S A A P S K K S K G C F K E			437
M.m. ADPRT	512	E G V N K S E R M K 522			511

Figure 1.

Figure 2.

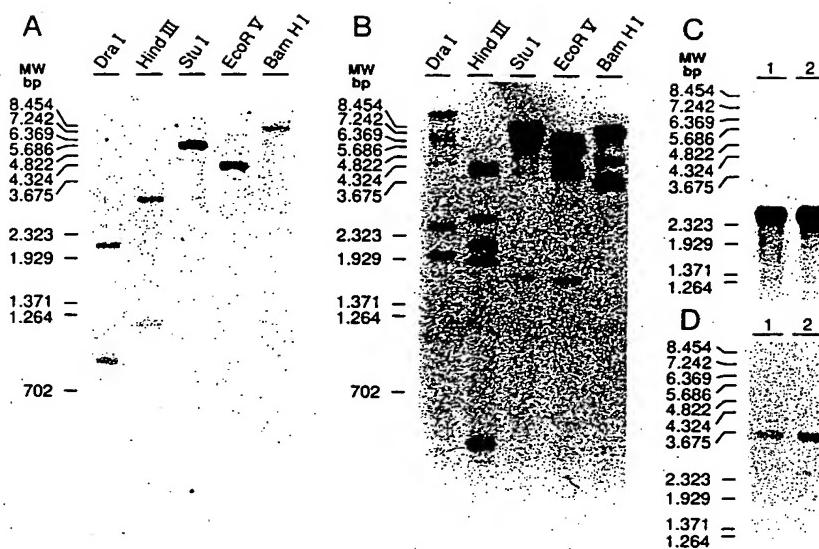


Figure 3.

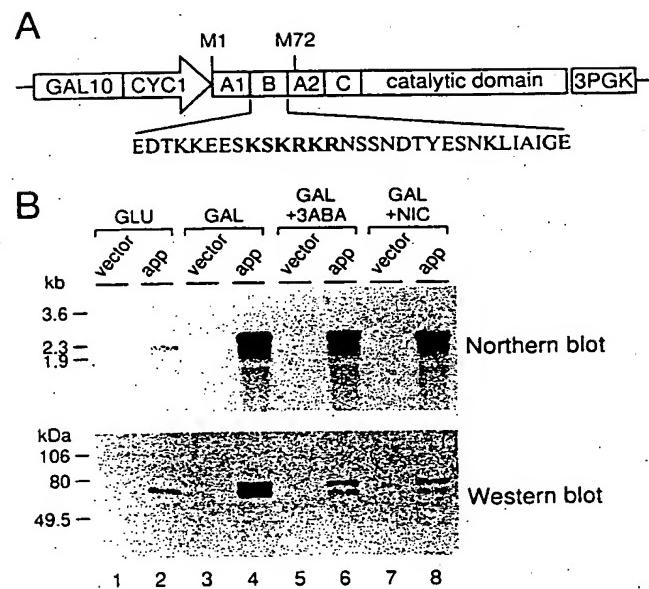


Figure 4

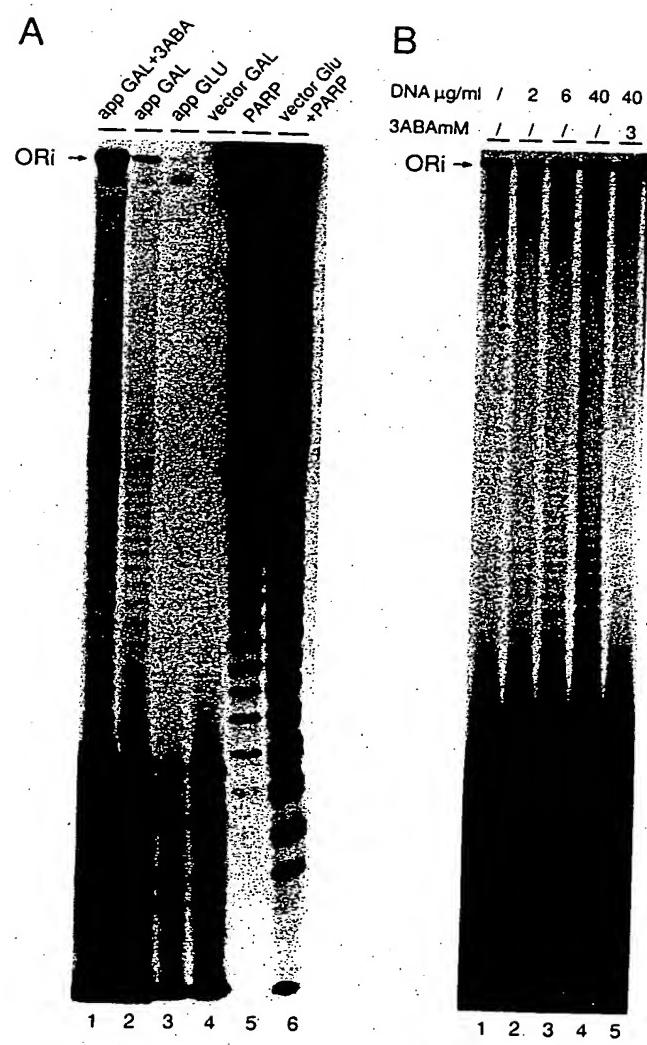


Figure 5.

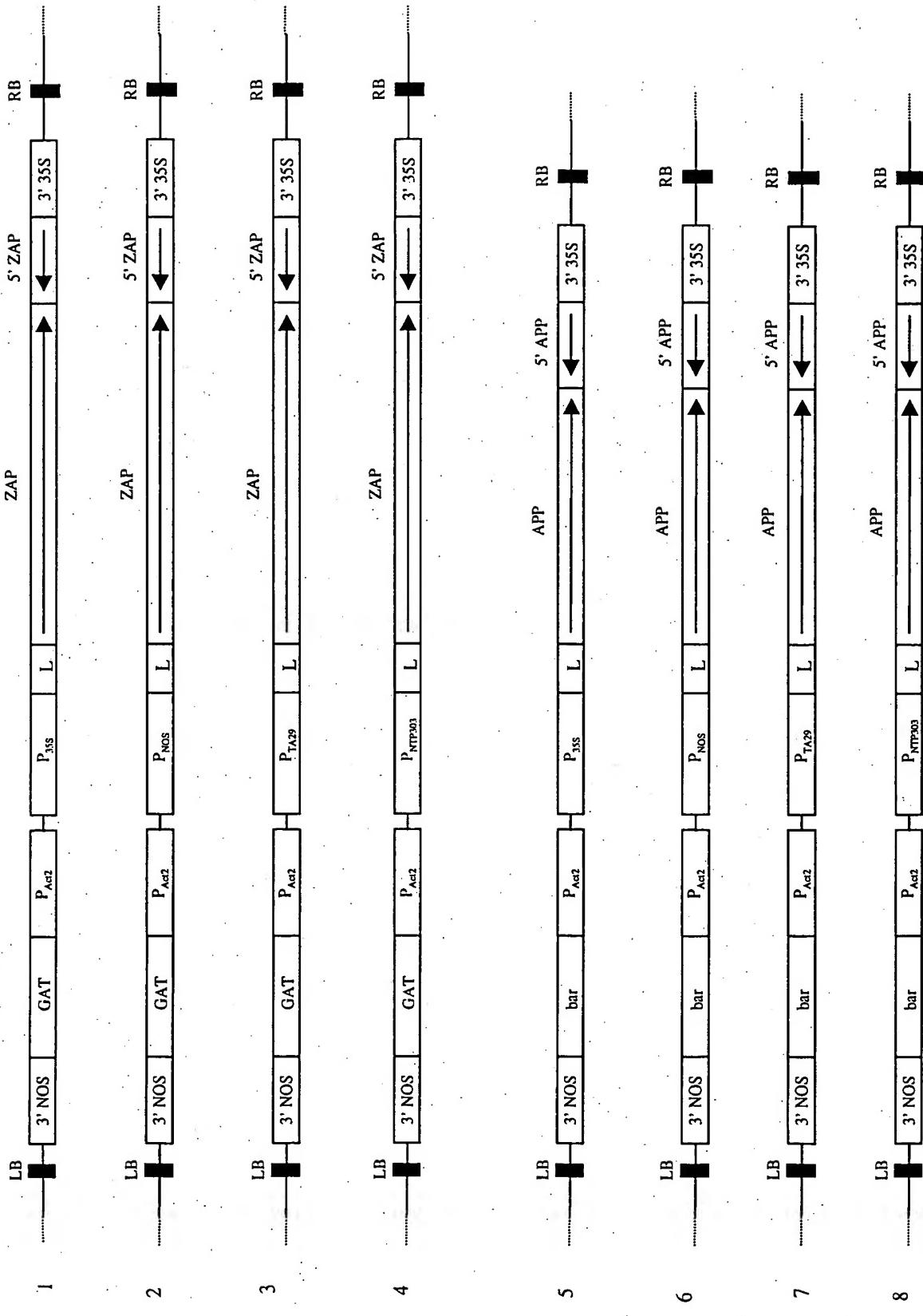


Figure 6